

Raw Sequence Listing
Patent Application US/07/621,092C

#13
06/04/91
12:11:55

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Kaufman, Randal J.
Wasley, Louise

(ii) TITLE OF INVENTION: Method of Increasing Yield of Mature
Proteins

(iii) NUMBER OF SEQUENCES: 2

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genetics Institute, Inc.
(B) STREET: 87 CambridgePark Drive
(C) CITY: Cambridge
(D) STATE: Massachusetts
(E) COUNTRY: U.S.A.
(F) ZIP: 02140

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/621,092
(B) FILING DATE: 26-NOV-1990
(C) CLASSIFICATION: 424

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Kapinos, Ellen J.
(B) REGISTRATION NUMBER: 32,245

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (617)876-1170
(B) TELEFAX: (617)876-5851

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2385 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

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54 (A) NAME/KEY: CDS
 55 (B) LOCATION: 1..2382
 56
 57 (x) PUBLICATION INFORMATION:
 58 (A) AUTHORS: van den Ouweland, A.M.W.
 59 (C) JOURNAL: Nucleic Acids Res.
 60 (D) VOLUME: 18
 61 (F) PAGES: 664-
 62 (G) DATE: 1990
 63
 64 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
 65
 66 ATG GAG CTC AGG CCC TGG TTC CTA TGG GTC GTA CCA CCA ACA GGA ACC 48
 67 Met Glu Leu Arg Pro Trp Phe Leu Trp Val Val Pro Pro Thr Gly Thr
 68 1 5 10 15
 69
 70 TTG GTC CTG CTA GCA GCT GAT GCT CAG GGC CAG AAG GTC TTC ACC AAC 96
 71 Leu Val Leu Leu Ala Ala Asp Ala Gln Gly Gln Lys Val Phe Thr Asn
 72 20 25 30
 73
 74 ACG TGG GCT GTG CGC ATC CCT GGA GGC CCA GCG GTG GCC AAC AGT GTG 144
 75 Thr Trp Ala Val Arg Ile Pro Gly Gly Pro Ala Val Ala Asn Ser Val
 76 35 40 45
 77
 78 GCA CGG AAG CAT GGG TTC CTC AAC CTG GGC CAG ATC TTC GGG GAC TAT 192
 79 Ala Arg Lys His Gly Phe Leu Asn Leu Gly Gln Ile Phe Gly Asp Tyr
 80 50 55 60
 81
 82 TAC CAC TTC TGG CAT CGA GGA GTG ACG AAG CGG TCC CTG TCG CCT CAC 240
 83 Tyr His Phe Trp His Arg Gly Val Thr Lys Arg Ser Leu Ser Pro His
 84 65 70 75 80
 85
 86 CGC CCG CGG CAC AGC CGG CTG CAG AGG GAG CCT CAA GTA CAG TGG CTG 288
 87 Arg Pro Arg His Ser Arg Leu Gln Arg Glu Pro Gln Val Gln Trp Leu
 88 85 90 95
 89
 90 GAA CAG CAG GTG GCA AAG CGA CGG ACT AAA CGG GAC GTG TAC CAG GAG 336
 91 Glu Gln Gln Val Ala Lys Arg Arg Thr Lys Arg Asp Val Tyr Gln Glu
 92 100 105 110
 93
 94 CCC ACA GAC CCC AAG TTT CCT CAG CAG TGG TAC CTG TCT GGT GTC ACT 384
 95 Pro Thr Asp Pro Lys Phe Pro Gln Gln Trp Tyr Leu Ser Gly Val Thr
 96 115 120 125
 97
 98 CAG CGG GAC CTG AAT GTG AAG GCG GCC TGG GCG CAG GGC TAC ACA GGG 432
 99 Gln Arg Asp Leu Asn Val Lys Ala Ala Trp Ala Gln Gly Tyr Thr Gly
 100 130 135 140
 101
 102 CAC GGC ATT CTG GTC TCC ATT CTG GAC GAT GGC ATC GAG AAG AAC CAC 480
 103 His Gly Ile Leu Val Ser Ile Leu Asp Asp Gly Ile Glu Lys Asn His
 104 145 150 155 160
 105
 106 CCC GAC TTG GCA GGC AAT TAT GAT CCT GGG GCC AGT TTT CAT GTC AAT 528

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107	Pro	Asp	Leu	Ala	Gly	Asn	Tyr	Asp	Pro	Gly	Ala	Ser	Phe	His	Val	Asn	
108					165					170					175		
109																	
110	GAC	CAG	GAC	CCT	GAC	CCC	CAG	CCT	CGG	TAC	ACA	CAG	ATG	AAT	GAC	AAC	576
111	Asp	Gln	Asp	Pro	Asp	Pro	Gln	Pro	Arg	Tyr	Thr	Gln	Met	Asn	Asp	Asn	
112				180					185					190			
113																	
114	AGG	CAC	GGC	ACA	CGG	TGT	GCG	GGG	GAA	GTG	GCT	GCC	GTG	GCC	AAC	AAC	624
115	Arg	His	Gly	Thr	Arg	Cys	Ala	Gly	Glu	Val	Ala	Ala	Val	Ala	Asn	Asn	
116			195					200					205				
117																	
118	CGT	GTC	TGT	GGT	GTA	GGT	GTG	GCC	TAC	AAC	GCC	CGC	ATT	GGA	GGG	GTC	672
119	Arg	Val	Cys	Gly	Val	Gly	Val	Ala	Tyr	Asn	Ala	Arg	Ile	Gly	Gly	Val	
120		210					215					220					
121																	
122	CGC	ATG	CTG	GAT	GGC	GAG	GTG	ACA	GAT	GCA	GTG	GAG	GCA	CGC	TCG	CTG	720
123	Arg	Met	Leu	Asp	Gly	Glu	Val	Thr	Asp	Ala	Val	Glu	Ala	Arg	Ser	Leu	
124	225					230					235					240	
125																	
126	GGC	CTG	AAC	CCC	AAC	CAC	ATC	CAC	ATC	TAC	AGT	GCC	AGC	TGG	GGC	CCC	768
127	Gly	Leu	Asn	Pro	Asn	His	Ile	His	Ile	Tyr	Ser	Ala	Ser	Trp	Gly	Pro	
128					245					250					255		
129																	
130	GAG	GAT	GAC	GGC	AAG	ACA	GTG	GAT	GGG	CCA	GCC	CGG	CTC	GCC	GAG	GAG	816
131	Glu	Asp	Asp	Gly	Lys	Thr	Val	Asp	Gly	Pro	Ala	Arg	Leu	Ala	Glu	Glu	
132				260					265					270			
133																	
134	GCC	TTC	TTC	CGT	GGG	CTT	AGC	CAG	GGC	CGA	GGG	GGG	CTG	GGC	TCC	ATC	864
135	Ala	Phe	Phe	Arg	Gly	Leu	Ser	Gln	Gly	Arg	Gly	Gly	Leu	Gly	Ser	Ile	
136			275					280					285				
137																	
138	TTT	GTC	TGG	GCC	TCG	GGG	AAC	GGG	GGG	CGG	GAA	CAT	GAC	AGC	TGC	AAC	912
139	Phe	Val	Trp	Ala	Ser	Gly	Asn	Gly	Gly	Arg	Glu	His	Asp	Ser	Cys	Asn	
140		290					295					300					
141																	
142	TGC	GAC	GGC	TAC	ACC	AAC	AGT	ATC	TAC	ACG	CTG	TCC	ATC	AGC	AGC	GCC	960
143	Cys	Asp	Gly	Tyr	Thr	Asn	Ser	Ile	Tyr	Thr	Leu	Ser	Ile	Ser	Ser	Ala	
144	305					310					315					320	
145																	
146	ACG	CAG	TTT	GGC	AAC	GTG	CCG	TGG	TAC	AGC	GAG	GCC	TGC	TCG	TCC	ACA	1008
147	Thr	Gln	Phe	Gly	Asn	Val	Pro	Trp	Tyr	Ser	Glu	Ala	Cys	Ser	Ser	Thr	
148					325					330					335		
149																	
150	CTG	GCC	ACG	ACC	TAC	AGC	AGT	GGC	AAC	CAG	AAT	GAG	AAG	CAG	ATC	GTG	1056
151	Leu	Ala	Thr	Thr	Tyr	Ser	Ser	Gly	Asn	Gln	Asn	Glu	Lys	Gln	Ile	Val	
152				340					345					350			
153																	
154	ACG	ACT	GAC	TTG	CGG	CAG	AAG	TGC	ACG	GAG	TCT	CAC	ACG	GGC	ACC	TCA	1104
155	Thr	Thr	Asp	Leu	Arg	Gln	Lys	Cys	Thr	Glu	Ser	His	Thr	Gly	Thr	Ser	
156			355					360					365				
157																	
158	GCC	TCT	GCC	CCC	TTA	GCA	GCC	GGC	ATC	ATT	GCT	CTC	ACC	CTG	GAG	GCC	1152
159	Ala	Ser	Ala	Pro	Leu	Ala	Ala	Gly	Ile	Ile	Ala	Leu	Thr	Leu	Glu	Ala	

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160	370	375	380	
161				
162	AAT AAG AAC CTC ACA TGG CGG GAC ATG CAA CAC CTG GTG GTA CAG ACC			1200
163	Asn Lys Asn Leu Thr Trp Arg Asp Met Gln His Leu Val Val Gln Thr			
164	385	390	395	400
165				
166	TCG AAG CCA GCC CAC CTC AAT GCC AAC GAC TGG GCC ACC AAT GGT GTG			1248
167	Ser Lys Pro Ala His Leu Asn Ala Asn Asp Trp Ala Thr Asn Gly Val			
168		405	410	415
169				
170	GGG CGG AAA GTG AGC CAC TCA TAT GGC TAC GGG CTT TTC GAC GCA GGC			1296
171	Gly Arg Lys Val Ser His Ser Tyr Gly Tyr Gly Leu Phe Asp Ala Gly			
172		420	425	430
173				
174	GCC ATG GTG GCC CTG GCC CAG AAT TGG ACC ACA GTC GCC CCC CAG CGG			1344
175	Ala Met Val Ala Leu Ala Gln Asn Trp Thr Thr Val Ala Pro Gln Arg			
176		435	440	445
177				
178	AAG TGC ATC ATC GAC ATC CTC ACC GAG CCC AAA GAC ATC GGG AAA CGG			1392
179	Lys Cys Ile Ile Asp Ile Leu Thr Glu Pro Lys Asp Ile Gly Lys Arg			
180		450	455	460
181				
182	CTC GAC CTC CGG AAC ACC GTG ACC GCG TCC CTG GGC GAG CCC AAC CAC			1440
183	Leu Asp Leu Arg Asn Thr Val Thr Ala Ser Leu Gly Glu Pro Asn His			
184	465	470	475	480
185				
186	ATC ACT CGG CTG GAG CAC GCT CAG GCG CGG CTC ACC CTG TCC TAT AAT			1488
187	Ile Thr Arg Leu Glu His Ala Gln Ala Arg Leu Thr Leu Ser Tyr Asn			
188		485	490	495
189				
190	CGC CGT GGC GAC CTG GCC ATC CAC CTG GTC AGC CCC ATG GGC ACC CGC			1536
191	Arg Arg Gly Asp Leu Ala Ile His Leu Val Ser Pro Met Gly Thr Arg			
192		500	505	510
193				
194	TCC ACC CTG CTG GCA GCC AGG CCA CAT GAC TAC TCC GCA GAT GGG TTT			1584
195	Ser Thr Leu Leu Ala Ala Arg Pro His Asp Tyr Ser Ala Asp Gly Phe			
196		515	520	525
197				
198	AAT GAC TGG GCC TTC ATG ACA ACT CAT TCC TGG GAT GAC GAT CCC TCT			1632
199	Asn Asp Trp Ala Phe Met Thr Thr His Ser Trp Asp Asp Asp Pro Ser			
200		530	535	540
201				
202	GGG GAG TGG GTC CTA GAG ATT GAA AAC ACC AGC GAA GCC AAC AAC TAT			1680
203	Gly Glu Trp Val Leu Glu Ile Glu Asn Thr Ser Glu Ala Asn Asn Tyr			
204	545	550	555	560
205				
206	GGG ACG CTG ACC AAC TCC ACC CTC GTA CTC TAT GGC ACC GCC CCT GAC			1728
207	Gly Thr Leu Thr Asn Ser Thr Leu Val Leu Tyr Gly Thr Ala Pro Asp			
208		565	570	575
209				
210	GGG CTC CCC GTA CCT CCA GAA AGC AGT GGC TGC AAG ACC CTC ACG TCC			1776
211	Gly Leu Pro Val Pro Pro Glu Ser Ser Gly Cys Lys Thr Leu Thr Ser			
212		580	585	590

213																		
214	AGT	CAG	GCC	TGT	GTG	GTG	TGC	GAG	GAA	GGC	TTC	TCC	CTC	CAC	CAG	AAG		1824
215	Ser	Gln	Ala	Cys	Val	Val	Cys	Glu	Glu	Gly	Phe	Ser	Leu	His	Gln	Lys		
216			595					600					605					
217																		
218	AGC	TGT	GTC	CAG	CAC	TGC	CCT	CCA	GGC	TTC	GCC	CCC	CAA	GTC	CTC	GAT		1872
219	Ser	Cys	Val	Gln	His	Cys	Pro	Pro	Gly	Phe	Ala	Pro	Gln	Val	Leu	Asp		
220		610					615					620						
221																		
222	ACG	CAC	TAT	AGC	ACC	GAG	AAT	GAC	GTG	GAG	ACC	ATC	CGG	GCC	AGC	GTC		1920
223	Thr	His	Tyr	Ser	Thr	Glu	Asn	Asp	Val	Glu	Thr	Ile	Arg	Ala	Ser	Val		
224	625					630					635					640		
225																		
226	TGC	GCC	CCC	TGC	CAC	GCC	TCA	TGT	GCC	ACA	TGC	CAG	GGG	CCG	GCC	CTG		1968
227	Cys	Ala	Pro	Cys	His	Ala	Ser	Cys	Ala	Thr	Cys	Gln	Gly	Pro	Ala	Leu		
228					645					650					655			
229																		
230	ACA	GAC	TGC	CTC	AGC	TGC	CCC	AGC	CAC	GCC	TCC	TTG	GAC	CCT	GTG	GAG		2016
231	Thr	Asp	Cys	Leu	Ser	Cys	Pro	Ser	His	Ala	Ser	Leu	Asp	Pro	Val	Glu		
232				660					665					670				
233																		
234	CAG	ACT	TGC	TCC	CGG	CAA	AGC	CAG	AGC	AGC	CGA	GAG	TCC	CCG	CCA	CAG		2064
235	Gln	Thr	Cys	Ser	Arg	Gln	Ser	Gln	Ser	Ser	Arg	Glu	Ser	Pro	Pro	Gln		
236			675					680					685					
237																		
238	CAG	CAG	CCA	CCT	CGG	CTG	CCC	CCG	GAG	GTG	GAG	GCG	GGG	CAA	CGG	CTG		2112
239	Gln	Gln	Pro	Pro	Arg	Leu	Pro	Pro	Glu	Val	Glu	Ala	Gly	Gln	Arg	Leu		
240		690					695					700						
241																		
242	CGG	GCA	GGG	CTG	CTG	CCC	TCA	CAC	CTG	CCT	GAG	GTG	GTG	GCC	GGC	CTC		2160
243	Arg	Ala	Gly	Leu	Leu	Pro	Ser	His	Leu	Pro	Glu	Val	Val	Ala	Gly	Leu		
244	705					710					715					720		
245																		
246	AGC	TGC	GCC	TTC	ATC	GTG	CTG	GTC	TTC	GTC	ACT	GTC	TTC	CTG	CTC	CTG		2208
247	Ser	Cys	Ala	Phe	Ile	Val	Leu	Val	Phe	Val	Thr	Val	Phe	Leu	Leu	Leu		
248					725					730					735			
249																		
250	CAG	CTG	CGC	TCT	GGC	TTT	AGT	TTT	CGG	GGG	GTG	AAG	GTG	TAC	ACC	ATG		2256
251	Gln	Leu	Arg	Ser														

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266

267 (2) INFORMATION FOR SEQ ID NO:2:

268

269 (i) SEQUENCE CHARACTERISTICS:

270 (A) LENGTH: 794 amino acids

271 (B) TYPE: amino acid

272 (D) TOPOLOGY: linear

273

274 (ii) MOLECULE TYPE: protein

275

276 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

277

278 Met Glu Leu Arg Pro Trp Phe Leu Trp Val Val Pro Pro Thr Gly Thr

279 1 5 10 15

280

281 Leu Val Leu Leu Ala Ala Asp Ala Gln Gly Gln Lys Val Phe Thr Asn

282 20 25 30

283

284 Thr Trp Ala Val Arg Ile Pro Gly Gly Pro Ala Val Ala Asn Ser Val

285 35 40 45

286

287 Ala Arg Lys His Gly Phe Leu Asn Leu Gly Gln Ile Phe Gly Asp Tyr

288 50 55 60

289

290 Tyr His Phe Trp His Arg Gly Val Thr Lys Arg Ser Leu Ser Pro His

291 65 70 75 80

292

293 Arg Pro Arg His Ser Arg Leu Gln Arg Glu Pro Gln Val Gln Trp Leu

294 85 90 95

295

296 Glu Gln Gln Val Ala Lys Arg Arg Thr Lys Arg Asp Val Tyr Gln Glu

297 100 105 110

298

299 Pro Thr Asp Pro Lys Phe Pro Gln Gln Trp Tyr Leu Ser Gly Val Thr

300 115 120 125

301

302 Gln Arg Asp Leu Asn Val Lys Ala Ala Trp Ala Gln Gly Tyr Thr Gly

303 130 135 140

304

305 His Gly Ile Leu Val Ser Ile Leu Asp Asp Gly Ile Glu Lys Asn His

306 145 150 155 160

307

308 Pro Asp Leu Ala Gly Asn Tyr Asp Pro Gly Ala Ser Phe His Val Asn

309 165 170 175

310

311 Asp Gln Asp Pro Asp Pro Gln Pro Arg Tyr Thr Gln Met Asn Asp Asn

312 180 185 190

313

314 Arg His Gly Thr Arg Cys Ala Gly Glu Val Ala Ala Val Ala Asn Asn

315 195 200 205

316

317 Arg Val Cys Gly Val Gly Val Ala Tyr Asn Ala Arg Ile Gly Gly Val

318 210 215 220

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319
320 Arg Met Leu Asp Gly Glu Val Thr Asp Ala Val Glu Ala Arg Ser Leu
321 225 230 235 240
322
323 Gly Leu Asn Pro Asn His Ile His Ile Tyr Ser Ala Ser Trp Gly Pro
324 245 250 255
325
326 Glu Asp Asp Gly Lys Thr Val Asp Gly Pro Ala Arg Leu Ala Glu Glu
327 260 265 270
328
329 Ala Phe Phe Arg Gly Leu Ser Gln Gly Arg Gly Gly Leu Gly Ser Ile
330 275 280 285
331
332 Phe Val Trp Ala Ser Gly Asn Gly Gly Arg Glu His Asp Ser Cys Asn
333 290 295 300
334
335 Cys Asp Gly Tyr Thr Asn Ser Ile Tyr Thr Leu Ser Ile Ser Ser Ala
336 305 310 315 320
337
338 Thr Gln Phe Gly Asn Val Pro Trp Tyr Ser Glu Ala Cys Ser Ser Thr
339 325 330 335
340
341 Leu Ala Thr Thr Tyr Ser Ser Gly Asn Gln Asn Glu Lys Gln Ile Val
342 340 345 350
343
344 Thr Thr Asp Leu Arg Gln Lys Cys Thr Glu Ser His Thr Gly Thr Ser
345 355 360 365
346
347 Ala Ser Ala Pro Leu Ala Ala Gly Ile Ile Ala Leu Thr Leu Glu Ala
348 370 375 380
349
350 Asn Lys Asn Leu Thr Trp Arg Asp Met Gln His Leu Val Val Gln Thr
351 385 390 395 400
352
353 Ser Lys Pro Ala His Leu Asn Ala Asn Asp Trp Ala Thr Asn Gly Val
354 405 410 415
355
356 Gly Arg Lys Val Ser His Ser Tyr Gly Tyr Gly Leu Phe Asp Ala Gly
357 420 425 430
358
359 Ala Met Val Ala Leu Ala Gln Asn Trp Thr Thr Val Ala Pro Gln Arg
360 435 440 445
361
362 Lys Cys Ile Ile Asp Ile Leu Thr Glu Pro Lys Asp Ile Gly Lys Arg
363 450 455 460
364
365 Leu Asp Leu Arg Asn Thr Val Thr Ala Ser Leu Gly Glu Pro Asn His
366 465 470 475 480
367
368 Ile Thr Arg Leu Glu His Ala Gln Ala Arg Leu Thr Leu Ser Tyr Asn
369 485 490 495
370
371 Arg Arg Gly Asp Leu Ala Ile His Leu Val Ser Pro Met Gly Thr Arg

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	500	505	510
372			
373			
374	Ser Thr Leu Leu Ala Ala Arg Pro His Asp Tyr Ser Ala Asp Gly Phe		
375	515	520	525
376			
377	Asn Asp Trp Ala Phe Met Thr Thr His Ser Trp Asp Asp Asp Pro Ser		
378	530	535	540
379			
380	Gly Glu Trp Val Leu Glu Ile Glu Asn Thr Ser Glu Ala Asn Asn Tyr		
381	545	550	555
382			
383	Gly Thr Leu Thr Asn Ser Thr Leu Val Leu Tyr Gly Thr Ala Pro Asp		
384	565	570	575
385			
386	Gly Leu Pro Val Pro Pro Glu Ser Ser Gly Cys Lys Thr Leu Thr Ser		
387	580	585	590
388			
389	Ser Gln Ala Cys Val Val Cys Glu Glu Gly Phe Ser Leu His Gln Lys		
390	595	600	605
391			
392	Ser Cys Val Gln His Cys Pro Pro Gly Phe Ala Pro Gln Val Leu Asp		
393	610	615	620
394			
395	Thr His Tyr Ser Thr Glu Asn Asp Val Glu Thr Ile Arg Ala Ser Val		
396	625	630	635
397			
398	Cys Ala Pro Cys His Ala Ser Cys Ala Thr Cys Gln Gly Pro Ala Leu		
399	645	650	655
400			
401	Thr Asp Cys Leu Ser Cys Pro Ser His Ala Ser Leu Asp Pro Val Glu		
402	660	665	670
403			
404	Gln Thr Cys Ser Arg Gln Ser Gln Ser Ser Arg Glu Ser Pro Pro Gln		
405	675	680	685
406			
407	Gln Gln Pro Pro Arg Leu Pro Pro Glu Val Glu Ala Gly Gln Arg Leu		
408	690	695	700
409			
410	Arg Ala Gly Leu Leu Pro Ser His Leu Pro Glu Val Val Ala Gly Leu		
411	705	710	715
412			
413	Ser Cys Ala Phe Ile Val Leu Val Phe Val Thr Val Phe Leu Leu Leu		
414	725	730	735
415			
416	Gln Leu Arg Ser Gly Phe Ser Phe Arg Gly Val Lys Val Tyr Thr Met		
417	740	745	750
418			
419	Asp Arg Gly Leu Ile Ser Tyr Lys Gly Leu Pro Pro Glu Ala Trp Gln		
420	755	760	765
421			
422	Glu Glu Cys Pro Ser Asp Ser Glu Glu Asp Glu Gly Arg Gly Glu Arg		
423	770	775	780
424			

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425 Thr Ala Phe Ile Lys Asp Gln Ser Ala Leu
426 785 790

PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/07/621,092C

DATE: 06/04/91
TIME: 12:12:27

LINE ERROR

ORIGINAL TEXT

29 Wrong application Serial Number
30 Wrong Filing Date
31 Wrong Classification

OK [

(A) APPLICATION NUMBER: US 07/621,092
(B) FILING DATE: 26-NOV-1990
(C) CLASSIFICATION: 424

PAGE: 1

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION US/07/621,092C

DATE: 06/04/91
TIME: 12:12:27

MANDATORY IDENTIFIER THAT WAS NOT FOUND

PRIOR APPLICATION DATA
APPLICATION NUMBER
FILING DATE

PAGE: 1

SEQUENCE CORRECTION REPORT
PATENT APPLICATION US/07/621,092C

DATE: 06/04/91
TIME: 12:12:27

LINE ORIGINAL TEXT

CORRECTED TEXT